



THE UNIVERSITY *of* EDINBURGH

Edinburgh Research Explorer

Complete genome sequence of a newly identified porcine astrovirus genotype 3 strain US-MO123

Citation for published version:

Xiao, C-T, Halbur, PG & Opriessnig, T 2012, 'Complete genome sequence of a newly identified porcine astrovirus genotype 3 strain US-MO123', *Journal of Virology*, vol. 86, no. 23, pp. 13126-13126.
<https://doi.org/10.1128/JVI.02426-12>

Digital Object Identifier (DOI):

[10.1128/JVI.02426-12](https://doi.org/10.1128/JVI.02426-12)

Link:

[Link to publication record in Edinburgh Research Explorer](#)

Document Version:

Publisher's PDF, also known as Version of record

Published In:

Journal of Virology

General rights

Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy

The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.



Complete Genome Sequence of a Newly Identified Porcine Astrovirus Genotype 3 Strain US-MO123

Chao-Ting Xiao, Patrick G. Halbur, and Tanja Opriessnig

Department of Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, Iowa, USA

Astrovirus (AstV) infections are among the most common causes of gastroenteritis and are also associated with extraintestinal manifestations in humans and many animals. Herein, for the first time, the complete genome sequence of newly identified porcine astrovirus genotype 3 (PAstV3) strain US-MO123 was determined. Sequence comparison and phylogenetic analysis showed that PAstV3 has the closest relationship with mink AstV and the human AstV strains VA1, VA2, and SG, indicating the same ancestral origin and zoonotic potential of the virus.

Astroviruses (AstV) are nonenveloped, single-stranded, positive-sense RNA viruses of the family of *Astroviridae* (3) and have been isolated from feces of a wide variety of mammals and birds (1, 3). In most species, these viruses are associated with gastroenteritis in young individuals; however, in some birds and animals, these viruses have been associated with extraintestinal diseases (1–4, 8). Since the first porcine astrovirus (PAstV) was detected in pigs in the 1980s (4), five genotypes of PAstV have been identified (6, 7, 9), but an association with clinical disease still remains unclear.

Herein, PAstV genotype 3 (PAstV3) RNA was identified by real-time PCR in a fecal sample of a pig suffering from diarrhea and subsequently sequenced with detection primers based on a conserved region. As PAstV3 may play a role in diarrhea or other clinical manifestations in pigs, the genome features of the PAstV3 strain designated US-MO123 were characterized.

First, the 3' partial genome of US-MO123 was obtained using primers based on the known partial genome of PAstV3. The 5' partial genome was obtained using degenerate primers based on the alignment of human and mink AstV genomes which previously showed the closest relationship to PAstV3 (9). The 5' and 3' terminals of the genome were acquired by using a rapid amplification of cDNA ends (RACE) kit (TaKaRa, Japan). The obtained complete genome of PAstV3 possesses a typical AstV organization, with a size of 6,430 bp excluding the poly(A) tail and a GC content of 47.1%. Three main open reading frames (ORFs) are predicted, with a short 5' untranslated region (UTR) of 30 bp and a 3' UTR of 82 bp. ORF1a (bp 31 to 2,565) and ORF2 (bp 3,895 to 6,348) encode proteins of 844 amino acids (aa) and 817 aa, respectively. Translation of ORF1b (bp 2,562 to 4,091) may be linked to ORF1a by a ribosomal frame-shifting mechanism, resulting in a polyprotein (ORF1ab) of 1,353 aa. The whole genome of US-MO123 shows low identities of 38.4% to 42.7% with the known genomes of PAstV1 (GenBank accession no. [GQ914773](#)), PAstV2 (GenBank accession no. [JF713710](#)), PAstV4 (GenBank accession no. [JF713713](#)), and PAstV5 (GenBank accession no. [JF713711](#)) and showed an identity of 91.8% with the only known partial genome of PAstV3 strain 16-2 (2,931 bp; GenBank accession no. [HM756261](#)).

Phylogenetic analysis based on the ORF2 gene sequences revealed that PAstV3 has the closest relationship with mink AstV and the human AstV strains VA1, VA2, and SG (9). Mink AstV was reported to be associated with shaking mink syndrome (2), while the human strain VA1 was associated with an outbreak of acute gastroenteritis in a child care center (5) and SG was reported as a causative agent for encephalitis in a boy with agammaglobu-

linemia (8). The genome of PAstV3 has higher identities of 50.5% to 55.3% with mink AstV and the human AstV strains VA1, VA2, and SG than with other PAstV genotypes, indicating the same origin for PAstV3, mink AstV, and human AstVs. However, the potential role of PAstV3 in clinical manifestations in pigs and the zoonotic potential need further investigation.

Nucleotide sequence accession number. The complete genome sequence of PAstV3 strain US-MO123 has been deposited in GenBank under the accession no. [JX556691](#).

ACKNOWLEDGMENT

This study was supported by the Iowa State University Veterinary Diagnostic Laboratory.

REFERENCES

1. Bidin M, Lojkić I, Tisljar M, Bidin Z, Majnarić D. 2012. Astroviruses associated with stunting and pre-hatching mortality in duck and goose embryos. *Avian Pathol.* 41:91–97.
2. Blomström AL, Widen F, Hammer AS, Belak S, Berg M. 2010. Detection of a novel astrovirus in brain tissue of mink suffering from shaking mink syndrome by use of viral metagenomics. *J. Clin. Microbiol.* 48:4392–4396.
3. Bosch A, et al. 2011. Family *Astroviridae*, p. 953–959. In King AMQ, Lefkowitz E, Adams MJ, Carstens EB (ed), *Virus taxonomy: classification and nomenclature of viruses*. Ninth report of the International Committee on the Taxonomy of Viruses. Elsevier Academic Press, New York, NY.
4. De Benedictis P, Schultz-Cherry S, Burnham A, Cattoli G. 2011. Astrovirus infections in humans and animals—molecular biology, genetic diversity, and interspecies transmissions. *Infect. Genet. Evol.* 11:1529–1544.
5. Finkbeiner SR, et al. 2009. Identification of a novel astrovirus (astrovirus VA1) associated with an outbreak of acute gastroenteritis. *J. Virol.* 83:10836–10839.
6. Laurin MA, Dastor M, L'Homme Y. 2011. Detection and genetic characterization of a novel pig astrovirus: relationship to other astroviruses. *Arch. Virol.* 156:2095–2099.
7. Luo Z, et al. 2011. Multiple novel and prevalent astroviruses in pigs. *Vet. Microbiol.* 149:316–323.
8. Quan PL, et al. 2010. Astrovirus encephalitis in boy with X-linked agammaglobulinemia. *Emerg. Infect. Dis.* 16:918–925.
9. Shan T, et al. 2011. The fecal virome of pigs on a high-density farm. *J. Virol.* 85:11697–11708.

Received 5 September 2012 Accepted 5 September 2012

Address correspondence to Tanja Opriessnig, tanjaopr@iastate.edu.

Copyright © 2012, American Society for Microbiology. All Rights Reserved.

[doi:10.1128/JVI.02426-12](https://doi.org/10.1128/JVI.02426-12)